



## RAW SEQUENCE LISTING

DATE: 04/07/2003

PATENT APPLICATION: US/09/720,383C

TIME: 08:02:21

Input Set : N:\AMC\US09720383C.raw

Output Set: N:\CRF4\04072003\I720383C.raw

ENTERED

p.6

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1 <110> APPLICANT: Stephen M. Allen
2   Gary M. Fader
3   Saverio Carl Falco
4   Anthony J. Kinney
5   Jonathan E. Lightner
6   Guo-Hua Miao
7   J. Antoni Rafalski
8   Catherine J. Thorpe
9 <120> TITLE OF INVENTION: Plant Cellulose Synthases
10 <130> FILE REFERENCE: BB-1170
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/720,383C
12 <141> CURRENT FILING DATE: 2000-12-21
13 <150> PRIOR APPLICATION NUMBER: 60/092,844
14 <151> PRIOR FILING DATE: 1998-07-14
15 <160> NUMBER OF SEQ ID NOS: 29
16 <170> SOFTWARE: Microsoft Office 97
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1221
20 <212> TYPE: DNA
21 <213> ORGANISM: Hordeum vulgare
22 <400> SEQUENCE: 1
23   gcacgaggat attcttactg ggtttaaaat gcacgaaga ggttgatatt caatctactg   60
24   catgccacca cgacctgtgt tcaagggttc tgcgccaatc aatctctctg accgtctcaa   120
25   tcaagttctc cgggtgggtc ttgggtcagt tgaattctg tttagcagac attgtcctat   180
26   ctggtacaat tacggtgggc ggttgaaact tctggagagg atggcttaca tcaacaccat   240
27   tgtttatcca ataacatccc ttccacttat cgctattgt gtgcttctg ctatctgtct   300
28   cctcaccaac aaatttatca ttcccgagat cagtaactat gctgggatgt tctttattct   360
29   tatgtttgcc tccatctttg ccacgggat attggagctg cgatggagtg gtgtcggcat   420
30   cgaggactgg tggagaaacg agcagttctg gttatttgt ggcacatctg cccatctttt   480
31   cgcagtgttc cagggtctgc tgaagggtgt ggccgggatt gacaccaact tcacggttac   540
32   ctcgaaggca aacgacgagg atggcgattt tgctgagtta tacgtgttca agtggaccag   600
33   tctctcatt cctccgacca cgtccttgt gattaacctg gtgggcatgg tggcaggcat   660
34   atcatatgcc atcaacagcg gttaccagt ttgggggtcca ctcttcggaa agctcttctt   720
35   ctcaatctgg gtgatcctcc atctctaccc ctctctcaag ggtctcatgg ggaagcagaa   780
36   ccgcacgcca accatcgtca ttgtttggtc catcctccta gcctccatct tctccctcct   840
37   gtgggtgaag atcgacctt tcatatccga taccagaaa gccgtcgcca tggggcagtg   900
38   tggcgtcaac tgctgatcgg cgccgaagag tatctgcccc cctcgtgtaa ataccggagg   960
39   ggggttgatg ggattttgtt gttgtagatg aagacggagt tttatgtaag ttattattgc  1020
40   cccttcgtgc tgagaagcac aaaccgtgaa gcctacgaaa cctgcagcgt acattgtgat  1080
41   tttttctccc ttttcttttc atctgtgata cctgttggtt ctctcttagag tatattatgt  1140
42   cagaacgtat ctatagttct atacacacta tgacaccaac tatttatata aggcagctgt  1200
43   tgcacaaact cttctgcaaa a                                     1221
45 <210> SEQ ID NO: 2

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46 <211> LENGTH: 304
47 <212> TYPE: PRT
48 <213> ORGANISM: Hordeum vulgare
49 <400> SEQUENCE: 2
50   His Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly Trp Ile
51       1           5           10           15
52   Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys Gly Ser Ala Pro
53           20           25           30
54   Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly
55           35           40           45
56   Ser Val Glu Ile Leu Phe Ser Arg His Cys Pro Ile Trp Tyr Asn Tyr
57       50           55           60
58   Gly Gly Arg Leu Lys Leu Leu Glu Arg Met Ala Tyr Ile Asn Thr Ile
59       65           70           75           80
60   Val Tyr Pro Ile Thr Ser Leu Pro Leu Ile Ala Tyr Cys Val Leu Pro
61           85           90           95
62   Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu Ile Ser Asn
63           100          105          110
64   Tyr Ala Gly Met Phe Phe Ile Leu Met Phe Ala Ser Ile Phe Ala Thr
65           115          120          125
66   Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu Asp Trp Trp
67       130          135          140
68   Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala His Leu Phe
69       145          150          155          160
70   Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp Thr Asn
71           165          170          175
72   Phe Thr Val Thr Ser Lys Ala Asn Asp Glu Asp Gly Asp Phe Ala Glu
73           180          185          190
74   Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro Thr Thr Val
75           195          200          205
76   Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser Tyr Ala Ile
77       210          215          220
78   Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe
79       225          230          235          240
80   Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys Gly Leu Met
81           245          250          255
82   Gly Lys Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu
83           260          265          270
84   Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp Pro Phe Ile
85           275          280          285
86   Ser Asp Thr Gln Lys Ala Val Ala Met Gly Gln Cys Gly Val Asn Cys
87       290          295          300
89 <210> SEQ ID NO: 3
90 <211> LENGTH: 3776
91 <212> TYPE: DNA
92 <213> ORGANISM: Zea mays
93 <400> SEQUENCE: 3
94   ggcgcgcgcg caggcgcaac gcaacaaagg gaaaccccag ccggaggagc aaaagctagc 60
95   aagcgtgtcc ctccccctcc ctcactcccg ttctattcca ttcccccca gacgccgcta 120

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96      ccgcgcgcgc cgcacgcacg cttgccccgg gatctggaga tctggtagcg ccaggggggat 180
97      ggaggccagc gccgggctgg tcgccggctc gcacaaccgg aacgagctcg tcgtcatccg 240
98      ccgcgatggc gagccagggc cgaagcccat ggaccagcgg aacggccagg tgtgccagat 300
99      ttgcggcgac gacgtggggc gcaaccccga cggggagccg ttcgtggcct gcaacgagtg 360
100     cgccctcccc atctgccggg actgctacga gtacgagcgc cgcgagggca cgcagaactg 420
101     cccccagtgc aagaccgcgt tcaagcgct caaggggtgc gcgcgcgtgc ccggggacga 480
102     ggaggaggac ggcgtcgacg acctggagaa cgagttcaac tggagcgaca agcacgactc 540
103     ccagtacctc gccgagtcga tgctccacgc ccacatgagc tacggcccgcg gcgccgacct 600
104     cgacggcggtg ccgcagccat tccaccccat ccccaatggt cccctcctca ccaacggaca 660
105     gatggtcgat gacatcccgc cggaccagca cgcccttggt ccctcgttcg tgggtggcgg 720
106     ggggaagagg attcaccctc tcccgtagc ggatcccaac ctctctgtgc aaccgaggtc 780
107     tatggacctc tccaaggatc tcgcgcgata tggctacggg agcgtagcat ggaagggagag 840
108     gatggagagc tggaagcaga agcaggagag gatgcaccag acgaggaacg atggcggcgg 900
109     cgatgatggt gatgatgcag atctaccact aatggatgaa gctagacagc cattgtccag 960
110     aaagatcccg cttccttcaa gccaaatcaa cccctatagg atgattataa taattcggct 1020
111     agtggttttg tgtttcttct tccactaccg agtgatgcac ccggtgcctg atgcatttgc 1080
112     tttatggctc atatctgtga tctgtgaaat ttggtttgcc atgtcttgga ttcttgacca 1140
113     gtttccaaag tggtttccta tcgagaggga aacctatctt gaccggctga gttaagggtt 1200
114     tgacaaggaa gggcatcctt ctcaactcgc ccctgttgat ttctttgtca gtacggttga 1260
115     tcccttgaag gaacctccat tggctactgc taatactggt ctatctatcc tttcggtgga 1320
116     ttatccagtt gataaggttt catgctacgt ttctgatgat ggtgctgcca tgctgacatt 1380
117     tgaagcattg tctgaaacat ctgaatttgc aaagaaatgg gttcctttct gcaaaaagata 1440
118     tagccttgag cctcgtgctc cacagtggta tctccaacag aagatagact acctgaaaga 1500
119     caaggtggcg ccaaactttg tttagaagcg gagagcaatg aagagagagt atgagaatt 1560
120     caaggtcaga atcaatgcct tggttgctaa agcccaaaag gttcctgagg aaggatggac 1620
121     aatgcaggat ggaactccat ggcccggaaa taatgtccgt gatcatcctg gaatgattca 1680
122     ggttttcctt ggtcaaagtg gtggccatga tgtggaagga aatgagctgc ctcgattggt 1740
123     ttatgtttca agagaaaaac ggccaggcta caaccatcac aagaaggctg gtgctatgaa 1800
124     tgcattggtc cgagtctctg ctgtactaac taatgtcctt tatttgctga acttgattg 1860
125     tgatcactat atcaataata gtaaggctat aaaggaagca atgtgtttta tgatggatcc 1920
126     tttgcttgga aagaaagttt gctatgtgca gtttcctcaa agatttgatg ggattgatcg 1980
127     ccatgatcga tatgctaaca gaaatgttgt ctttttcgat atcaacatga aaggtttgga 2040
128     tggtatccag ggcccaattt atgtgggtac tggatgtgtc ttcagaaggc aggcattata 2100
129     tggttacgat gctcccaaaa caaagaagcc accatcaaga acttgcaact gctggccaaa 2160
130     gtgggtgcatt tgctgttgct gttttggtaa caggaagacc aagaagaaga ccaagacctc 2220
131     taaacctaaa tttgagaaga taaagaaact ttttaagaaa aaggaaaatc aagccctgc 2280
132     atatgtctct ggtgaaattg atgaagccgc tccaggagct gaaaatgaaa aggctagtat 2340
133     tgtaaatcaa cagaagttgg aaaagaaatt tggccagtct tcagtttttg ttgcatccac 2400
134     acttcttgag aatggtggaa ccctgaagag tggcagtcca gttctcttc tgaaggagc 2460
135     tatacatgtc atcagttgtg gatatgaaga caaacaggc tggggaaaag atattggttg 2520
136     gatttatgga tcagtcacag aagatattct tactgggttt aagatgcact gccatggttg 2580
137     gcggtcaatt tactgcatac ctaaacggcg cgccctcaaa ggttcgcgac ctctcaatct 2640
138     ttccgatcgt cttcaccagg ttcttcggtg ggctcttggt tcaattgaaa tttcttcag 2700
139     caaccactgc cctctctggt atgggtatgg tgggtgacta aagttcctgg aaaggttttc 2760
140     gtacattaac tccatcgat acccttgac atctatcccg ctcttgccct attgcacatt 2820
141     gcctgccatc tgcttgctga cagggaatt tatcacgcca gagcttaaca atgttgccag 2880
142     cctctggttc atgtcacttt tcatctgcag ttttgctacg agcatcctgg aaatgagatg 2940
143     gagtgggtga ggcacgatg actgtggag aaacgagcag ttttgggtca ttggaggcgt 3000
144     gtcttcacat ctctttgctg tgttcaggcg actcctcaag gtcatagctg gtgtagacac 3060

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145 gagcttcact gtgacatcca agggcggaga cgacgaggag ttctcagagc tgtacacatt 3120
146 caaatggacg acccttctga tacctccgac aacctgctc ctactgaact tcattggagt 3180
147 ggtagctggc atctccaatg cgatcaacaa cggatatgaa tcatggggcc ccctgttcgg 3240
148 gaagctcttc tttgcatttt ggggtatcgt ccatctttac ccgttctca aggggtctgg 3300
149 tgggaggcag aacaggacgc caacgattgt cattgtctgg tccatcctcc tggcttcgat 3360
150 cttctcgctg ctttgggtcc ggatcgaccc gttccttgcg aaggatgatg gtcccctgtt 3420
151 ggaggagtgt ggtctggatt gcaactagga ggtcagcacg tggacttccc cgtcagtgtg 3480
152 tggtcgaaga agtatttttg cagatgtttt gtgcccataat ttcttttttc aatttttgtc 3540
153 cctctgtaga tagaaacaag gggagaaggg gaaaaaaagt acttgtattt cttttgttcc 3600
154 atgggtgggg tgggtggggg cggctcagcc tcgtgagtg agtattgggc aaaccggagg 3660
155 ctgcggaac cttgtgcagt tcggccacga atatactagg gaagatcgcg accaatcaat 3720
156 caatcgatga ccgagttcaa ttgttcagca aaaaaaaaaa aaaaaaaaaa aaaaaa 3776
158 <210> SEQ ID NO: 4
159 <211> LENGTH: 1148
160 <212> TYPE: PRT
161 <213> ORGANISM: Zea mays
162 <400> SEQUENCE: 4
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164 1 5 10 15
165 Gln Lys Leu Ala Ser Val Ser Leu Pro Leu Pro His Ser Arg Phe Ile
166 20 25 30
167 Pro Phe Pro Pro Arg Arg Arg Tyr Arg Arg Arg Arg Thr His Ala Cys
168 35 40 45
169 Pro Gly Ile Trp Arg Ser Gly Ser Ala Arg Gly Met Glu Ala Ser Ala
170 50 55 60
171 Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu Leu Val Val Ile Arg
172 65 70 75 80
173 Arg Asp Gly Glu Pro Gly Pro Lys Pro Met Asp Gln Arg Asn Gly Gln
174 85 90 95
175 Val Cys Gln Ile Cys Gly Asp Asp Val Gly Arg Asn Pro Asp Gly Glu
176 100 105 110
177 Pro Phe Val Ala Cys Asn Glu Cys Ala Phe Pro Ile Cys Arg Asp Cys
178 115 120 125
179 Tyr Glu Tyr Glu Arg Arg Glu Gly Thr Gln Asn Cys Pro Gln Cys Lys
180 130 135 140
181 Thr Arg Phe Lys Arg Leu Lys Gly Cys Ala Arg Val Pro Gly Asp Glu
182 145 150 155 160
183 Glu Glu Asp Gly Val Asp Asp Leu Glu Asn Glu Phe Asn Trp Ser Asp
184 165 170 175
185 Lys His Asp Ser Gln Tyr Leu Ala Glu Ser Met Leu His Ala His Met
186 180 185 190
187 Ser Tyr Gly Arg Gly Ala Asp Leu Asp Gly Val Pro Gln Pro Phe His
188 195 200 205
189 Pro Ile Pro Asn Val Pro Leu Leu Thr Asn Gly Gln Met Val Asp Asp
190 210 215 220
191 Ile Pro Pro Asp Gln His Ala Leu Val Pro Ser Phe Val Gly Gly Gly
192 225 230 235 240
193 Gly Lys Arg Ile His Pro Leu Pro Tyr Ala Asp Pro Asn Leu Pro Val
194 245 250 255

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195   Gln Pro Arg Ser Met Asp Pro Ser Lys Asp Leu Ala Ala Tyr Gly Tyr
196           260           265           270
197   Gly Ser Val Ala Trp Lys Glu Arg Met Glu Ser Trp Lys Gln Lys Gln
198           275           280           285
199   Glu Arg Met His Gln Thr Arg Asn Asp Gly Gly Gly Asp Asp Gly Asp
200           290           295           300
201   Asp Ala Asp Leu Pro Leu Met Asp Glu Ala Arg Gln Pro Leu Ser Arg
202           305           310           315           320
203   Lys Ile Pro Leu Pro Ser Ser Gln Ile Asn Pro Tyr Arg Met Ile Ile
204           325           330           335
205   Ile Ile Arg Leu Val Val Leu Cys Phe Phe Phe His Tyr Arg Val Met
206           340           345           350
207   His Pro Val Pro Asp Ala Phe Ala Leu Trp Leu Ile Ser Val Ile Cys
208           355           360           365
209   Glu Ile Trp Phe Ala Met Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp
210           370           375           380
211   Phe Pro Ile Glu Arg Glu Thr Tyr Leu Asp Arg Leu Ser Leu Arg Phe
212           385           390           395           400
213   Asp Lys Glu Gly His Pro Ser Gln Leu Ala Pro Val Asp Phe Phe Val
214           405           410           415
215   Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Val Thr Ala Asn Thr
216           420           425           430
217   Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp Lys Val Ser Cys
218           435           440           445
219   Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Glu Ala Leu Ser
220           450           455           460
221   Glu Thr Ser Glu Phe Ala Lys Lys Trp Val Pro Phe Cys Lys Arg Tyr
222           465           470           475           480
223   Ser Leu Glu Pro Arg Ala Pro Glu Trp Tyr Phe Gln Gln Lys Ile Asp
224           485           490           495
225   Tyr Leu Lys Asp Lys Val Ala Pro Asn Phe Val Arg Glu Arg Arg Ala
226           500           505           510
227   Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn Ala Leu Val
228           515           520           525
229   Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Gln Asp Gly
230           530           535           540
231   Thr Pro Trp Pro Gly Asn Asn Val Arg Asp His Pro Gly Met Ile Gln
232           545           550           555           560
233   Val Phe Leu Gly Gln Ser Gly Gly His Asp Val Glu Gly Asn Glu Leu
234           565           570           575
235   Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Tyr Asn His
236           580           585           590
237   His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala Val
238           595           600           605
239   Leu Thr Asn Ala Pro Tyr Leu Leu Asn Leu Asp Cys Asp His Tyr Ile
240           610           615           620
241   Asn Asn Ser Lys Ala Ile Lys Glu Ala Met Cys Phe Met Met Asp Pro
242           625           630           635           640
243   Leu Leu Gly Lys Lys Val Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; Xaa Pos. 201

Seq#:19; N Pos. 262

Seq#:20; Xaa Pos. 88